



Research We Fund



Project:

Heritable methylation marks associated with bowel cancer risk

Research team:

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Institution: University Melbourne

Cancer type: Bowel cancer

Years funded: 2019–2020

What is the project?

Methylation is a type of ‘mark’ on DNA that can affect a person’s risk of cancer. Most methylation is erased soon after conception, but some methylation marks are effectively inherited from parents to their offspring. We have recently developed a new method to search for these heritable methylation marks. In a previous study, we used this new method to find 24 heritable methylation marks that are associated with an increased risk of breast cancer. We now aim to apply our innovative and successful methods to bowel cancer.

What is the need?

Identifying heritable methylation marks that are associated with an increased risk of bowel cancer will help to explain the cancers in some bowel cancer-prone families, who often do not have any known cause for their cancer.

In future work, the identified methylation marks can be incorporated into risk-prediction programs or used to suggest new drugs. Lastly, an aim of our study is to make our new methods publicly available, which will allow other researchers to apply our new and successful approach to many other diseases.

What are you trying to achieve?

I want to identify the cause of cancer in some families who have many cases of bowel cancer but no known cause for their cancer susceptibility. I also aim to make our methods available to other researchers so that they can discover heritable causes of many other diseases.

Project timeline

Timeline	2019	2020
Prepare and transport DNA. Measure methylation, including quality control.		
Analyse methylation data, write high-performance computer program implementing our new statistical method.		

“I want to identify the cause of cancer in some families who have many cases of bowel cancer but no known cause for their cancer susceptibility.”

